

SEQUENCE LISTING

<110> Reed, John C.  
Pio, Frederick F.  
Godzik, Adam  
Stehlik, Christian  
Damiano, Jason S.  
Lee, Sug-Hyung  
Oliveira, Vasco A.  
Hayashi, Hideki  
Pawlowski, Krzysztof

<120> Novel Card Domain Containing  
Polypeptides, Encoding Nucleic Acids, and Methods of Use

<130> P-LJ 4752

<150> US 09/579,240

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Patented by the United States Patent and Trademark Office

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FOR THE COURT



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Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
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Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr Asn Val Leu
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agc cag gaa gac aca gag ata gta aaa tgt gaa aat gtt aca gtt atc 144
Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile
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Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly
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gca tgt gaa att tgc atc aca tac att tgt gaa gaa gac agg tac ctg 240
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"F06250" F06250

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 Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile  
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 Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly  
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 Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu  
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                     35                    40                    45  
 Val Ile Asp Lys Ala Arg Ala Leu Leu Asp Ser Val Ile Arg Lys Gly  
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 Ala Gly Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Ser  
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 Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Ala Val Gln Ala  
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 Gly Gly Ala Cys Ser Thr Ser Ser Gly Gln Asp Leu  
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1264550









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Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile	
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Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser	
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745 750 755	
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825 830 835	
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ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat	2982
Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His	
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ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac 3078  
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920 925 930

cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc 3126  
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955 960 965

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Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu  
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Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu  
65 70 75 80  
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly  
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Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro  
100 105 110

CCDS: F04545.1

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Leu	Gln	Ser	Pro	Cys	Ile	Ile	Glu	Gly	Glu	Ser	Gly	Lys	Gly	Lys	Ser
				165					170					175	
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Tyr	Thr	Ala	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro
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TC330-TC335



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	75		80		85											
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Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys																
	90		95		100											
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Val Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp	
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315

320

325

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330 335 340

gat gat gat gat ctc agt gtt att aca ggt gct ttt aaa cta gta act 1350  
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<212> PRT

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Phe Gln Asp Leu Asn Gly Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn  
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115 120 125  
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Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile  
145 150 155 160  
Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala  
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Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu  
180 185 190  
Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp  
195 200 205  
Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly  
210 215 220  
Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu  
225 230 235 240  
Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp  
245 250 255

TC254250

Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys  
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275 280 285  
Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln Leu Val Phe  
290 295 300  
Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala Leu Val Arg  
305 310 315 320  
Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg  
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Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
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Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val  
25 30 35  
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438  
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile  
40 45 50  
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Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu  
55 60 65 70  
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534  
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly  
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Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu  
50 55 60  
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acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180  
aaaagaggac aatattggga tcacctttga cctttccatt tggaaataat attttctatt 240  
gtgttataga aaggtgggaa gctttcatcc agaaca atg aat ttc ata aag gac 294  
Met Asn Phe Ile Lys Asp  
1 5  
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342  
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln  
10 15 20  
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390  
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val  
25 30 35  
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438

CCDS: P25499.1



115 120 125  
 Asn Leu Lys Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln  
 130 135 140  
 His His His Arg Val Glu Gln Leu Thr Leu Val Leu  
 145 150 155

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 aagaagagac ggctgcttat caat 24

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 ccacagcagg cctcgaagat gatc 24

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 Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu  
 1 5 10 15  
 Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu  
 20 25 30  
 Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly  
 35 40 45  
 Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu

RefSeq: T26433.6

50	55	60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala		
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Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly		80
	85	90
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His		95
	100	105
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu		110
	115	120
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu		125
	130	135
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu		140
	145	150
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln		155
	165	170
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala		175
	180	185
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln		190
	195	200
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu		205
	210	215
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met		220
	225	230
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu		235
	245	250
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val		255
	260	265
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His		270
	275	280
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe		285
	290	295
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val		300
	305	310
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu		315
	325	330
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr		335
	340	345
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg		350
	355	360
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn		365
	370	375
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser		380
	385	390
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu		395
	405	410
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg		415
	420	425
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu		430
	435	440
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser		445
	450	455
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly		460
	465	470
		475
		480

TC230 "TC4350"



	900		905		910										
His	Leu	Gln	Asp	Glu	Gly	Val	Cys	Ser	Leu	Ala	Glu	Gly	Leu	Lys	Lys
	915						920					925			
Asn	Ser	Ser	Leu	Lys	Ile	Leu	Asn	Ile	Lys	Ile	His	Ala	Ser	Gly	Phe
	930						935					940			
Asn	Lys	Leu	Leu	Glu	Ser	Ile	Phe	Cys	Ile	Leu	Leu	Val	Val	Glu	Ala
945						950				955					960
Phe	Phe	Leu	Gln	Lys	Val	Val	Lys	Ile	Leu	Glu	Glu	Met	Val	Val	Ser
			965						970					975	
Trp	Leu	Glu	Val	Arg	Leu	Ser	Asn	Asn	Cys	Ile	Thr	Tyr	Leu	Gly	Ala
			980				985						990		
Glu	Ala	Leu	Leu	Gln	Ala	Leu	Glu	Arg	Asn	Asp	Thr	Ile	Leu	Glu	Val
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Trp															

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FEEDBACK

TABLE 10

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U.S. Pat. 4,240,000

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ccactcgagc taatttccag gtatcggacc

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<223> primer

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gaagacagtt acctggcaga

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ttgtattctg aacatggcac c

21

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gatcatcatc caggccgccc gtggtgacag ccctgg

36

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ccagggctgt caccacgggc ggcttgatg atgac

36

<210> 151

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<400> 151

cggaattcat ggccgacaag gtcctg

26

<210> 152

<211> 38

<212> DNA

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cgctcgagtt agtcttgcat attaaggtaa tttccaga

38

<210> 153

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catgtgaatg atccctctag cag

23

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Sequence

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acgatagccg agcccttatt c 21

<210> 156  
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<400> 156  
gtatggaatg ttctgaatcg c 21

<210> 157  
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<212> DNA  
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<400> 159  
ggtggagcag gatgctgcta gagg 24

Sequence

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catcatttgc tgcgagaagg tggag 25

<210> 162  
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ttaacttgga taacacttgg ctaag 25

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<400> 163  
gtaaacatca ttgctgcga gaa 23

<210> 164  
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<220>  
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Patented Feb 23, 2000

<400> 164  
cccgggcagg tagaagatgc tat 23

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<400> 165  
aatttcataa aggacaatag ccgag 25

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tgtctactgt acttttctaag ctggt 25

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Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu  
1 5 10 15

gaa atc ctt caa cat gat cct gat tct atc tta gac acg tta act tct 96  
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser  
20 25 30

cgg agg ctg att tct gag gaa gag tat gag act ctg gag aat gtt aca 144  
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr  
35 40 45

gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta cag aaa aag 192  
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys  
50 55 60

gga gag gcg acc tgt cag cat ttt ctc aag tgt 225  
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys

65

70

75

<210> 168

<211> 75

<212> PRT

<213> Homo sapiens

<400> 168

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Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
 1           5           10           15
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
          20           25           30
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
          35           40           45
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
          50           55           60
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys
65           70           75

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<211> 228

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<213> Homo sapiens

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atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag      48
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
 1           5           10           15

ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg      96
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
          20           25           30

ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac      144
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
          35           40           45

ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc      192
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
          50           55           60

gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc                        228
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
65           70           75

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<210> 170

12549660

<211> 76  
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<213> Homo sapiens

<400> 170  
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu  
1 5 10 15  
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp  
20 25 30  
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His  
35 40 45  
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr  
50 55 60  
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu  
65 70 75

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<212> DNA  
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<220>  
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cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg ctc 48  
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu  
1 5 10 15  
  
cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt ttc 96  
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe  
20 25 30  
  
gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca ccg 144  
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro  
35 40 45  
  
tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg aat 192  
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn  
50 55 60  
  
gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc cca 240  
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro  
65 70 75 80  
  
ttg 243  
Leu

<210> 172

TC26430 "TC26430"

<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 172  
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu  
1 5 10 15  
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe  
20 25 30  
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro  
35 40 45  
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn  
50 55 60  
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro  
65 70 75 80  
Leu

<210> 173  
<211> 888  
<212> DNA  
<213> Homo sapiens

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gac gat gcg gac act gtg ctg gtg gtg ggt gag gcg ggc agt ggc aag 48  
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys  
1 5 10 15  
  
agc acg ctc ctg cag cgg ctg cac ttg ctg tgg gct gca ggg caa gac 96  
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp  
20 25 30  
  
ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg cag 144  
Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln  
35 40 45  
  
tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac tgc 192  
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys  
50 55 60  
  
tgt tgg cct gat gtt ggt caa gaa gac atc ttc cag tta ctc ctt gac 240  
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp  
65 70 75 80  
  
cac cct gac cgt gtc ctg tta acc ttt gat ggc ttt gac gag ttc aag 288  
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys  
85 90 95

FEEDBACK



<210> 174  
 <211> 296  
 <212> PRT  
 <213> Homo sapiens

<400> 174  
 Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys  
 1 5 10 15  
 Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp  
 20 25 30  
 Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln  
 35 40 45  
 Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys  
 50 55 60  
 Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp  
 65 70 75 80  
 His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys  
 85 90 95  
 Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr  
 100 105 110  
 Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys  
 115 120 125  
 Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe  
 130 135 140  
 Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu  
 145 150 155 160  
 Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val  
 165 170 175  
 Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly  
 180 185 190  
 Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln  
 195 200 205  
 Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr Thr Thr Asp Met  
 210 215 220  
 Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp  
 225 230 235 240  
 Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro  
 245 250 255  
 Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys  
 260 265 270  
 Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro  
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 Asp Asp Ile Ser Leu Gly Phe Leu  
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174 296 175 1209 DNA





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<400> 176

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Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser	Trp	Met	Val	Ser
			20					25					30		
Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly	Ser	Pro	Lys	Thr
		35					40					45			
Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe	Leu	Leu	His	Ala
	50					55					60				
Thr	Pro	Pro	Asp	Ser	Ala	Ser	Gln	Gly	Leu	Gly	Pro	Ser	Leu	Leu	Arg
65					70					75					80
Gly	Arg	Leu	Pro	Thr	Leu	Leu	His	Leu	Gly	Arg	Leu	Ala	Leu	Trp	Gly
				85					90					95	
Leu	Gly	Met	Cys	Cys	Tyr	Val	Phe	Ser	Ala	Gln	Gln	Leu	Gln	Ala	Ala
			100					105					110		
Gln	Val	Ser	Pro	Asp	Asp	Ile	Ser	Leu	Gly	Phe	Leu	Val	Arg	Ala	Lys
		115					120					125			
Gly	Val	Val	Pro	Gly	Ser	Thr	Ala	Pro	Leu	Glu	Phe	Leu	His	Ile	Thr
	130					135					140				
Phe	Gln	Cys	Phe	Phe	Ala	Ala	Phe	Tyr	Leu	Ala	Leu	Ser	Ala	Asp	Val
145					150					155					160
Pro	Pro	Ala	Leu	Leu	Arg	His	Leu	Phe	Asn	Cys	Gly	Arg	Pro	Gly	Asn
				165					170					175	
Ser	Pro	Met	Ala	Arg	Leu	Leu	Pro	Thr	Met	Cys	Ile	Gln	Ala	Ser	Glu
			180					185					190		
Gly	Lys	Asp	Ser	Ser	Val	Ala	Ala	Leu	Leu	Gln	Lys	Ala	Glu	Pro	His
		195					200					205			
Asn	Leu	Gln	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu	Leu	Ser	Arg	Glu
	210					215					220				
His	Trp	Gly	Leu	Leu	Ala	Glu	Cys	Gln	Thr	Ser	Glu	Lys	Ala	Leu	Leu
225					230					235					240
Arg	Arg	Gln	Ala	Cys	Ala	Arg	Trp	Cys	Leu	Ala	Arg	Ser	Leu	Arg	Lys
			245					250						255	
His	Phe	His	Ser	Ile	Pro	Pro	Ala	Ala	Pro	Gly	Glu	Ala	Lys	Ser	Val
		260						265					270		
His	Ala	Met	Pro	Gly	Phe	Ile	Trp	Leu	Ile	Arg	Ser	Leu	Tyr	Glu	Met
		275					280					285			
Gln	Glu	Glu	Arg	Leu	Ala	Arg	Lys	Ala	Ala	Arg	Gly	Leu	Asn	Val	Gly
	290					295					300				
His	Leu	Lys	Leu	Thr	Phe	Cys	Ser	Val	Gly	Pro	Thr	Glu	Cys	Ala	Ala
305					310					315					320
Leu	Ala	Phe	Val	Leu	Gln	His	Leu	Arg	Arg	Pro	Val	Ala	Leu	Gln	Leu
			325					330						335	
Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln	Leu	Leu	Pro	Cys
		340						345				350			
Leu	Gly	Val	Cys	Lys	Ala	Leu	Tyr	Leu	Arg	Asp	Asn	Asn	Ile	Ser	Asp

CCDS: P34240

355	360	365
Arg Gly Ile Cys Lys Leu	Ile Glu Cys Ala Leu	His Cys Glu Gln Leu
370	375	380
Gln Lys Leu Ala Leu Gly	Asn Asn Tyr Ile Thr	Ala Ala Gly Ala Gln
385	390	395
Val Leu Ala		400

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 <213> Homo sapiens

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atg act gtt ata aag caa atc aca gat gac cta ttt gta tgg aat gtt	96
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val	
20 25 30	
ctg aat cgc gaa gaa gta aac atc att tgc tgc gag aag gtg gag cag	144
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln	
35 40 45	
gat gct gct aga ggg atc att cac atg att ttg aaa aag ggt tca gag	192
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu	
50 55 60	
tcc tgt aac ctc ttt ctt aaa tcc ctt aag gag tgg aac tat cct cta	240
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu	
65 70 75 80	
ttt cag gac ttg aat gga caa	261
Phe Gln Asp Leu Asn Gly Gln	
85	

<210> 178  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 178

Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val

TC2250 "F04B60

	20		25		30										
Leu	Asn	Arg	Glu	Glu	Val	Asn	Ile	Ile	Cys	Cys	Glu	Lys	Val	Glu	Gln
	35		40		45										
Asp	Ala	Ala	Arg	Gly	Ile	Ile	His	Met	Ile	Leu	Lys	Lys	Gly	Ser	Glu
	50		55		60										
Ser	Cys	Asn	Leu	Phe	Leu	Lys	Ser	Leu	Lys	Glu	Trp	Asn	Tyr	Pro	Leu
65			70		75										80
Phe	Gln	Asp	Leu	Asn	Gly	Gln									
			85												

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 <222> (1)...(891)

<400> 179

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Leu	Gln	Ser	Pro	Cys	Ile	Ile	Glu	Gly	Glu	Ser	Gly	Lys	Gly	Lys	Ser	
1				5					10					15		
act	ctg	ctg	cag	cgc	att	gcc	atg	ctc	tgg	ggc	tcc	gga	aag	tgc	aag	96
Thr	Leu	Leu	Gln	Arg	Ile	Ala	Met	Leu	Trp	Gly	Ser	Gly	Lys	Cys	Lys	
			20					25					30			
gct	ctg	acc	aag	ttc	aaa	ttc	gtc	ttc	ttc	ctc	cgt	ctc	agc	agg	gcc	144
Ala	Leu	Thr	Lys	Phe	Lys	Phe	Val	Phe	Phe	Leu	Arg	Leu	Ser	Arg	Ala	
		35					40					45				
cag	ggt	gga	ctt	ttt	gaa	acc	ctc	tgt	gat	caa	ctc	ctg	gat	ata	cct	192
Gln	Gly	Gly	Leu	Phe	Glu	Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro	
	50					55					60					
ggc	aca	atc	agg	aag	cag	aca	ttc	atg	gcc	atg	ctg	ctg	aag	ctg	cgg	240
Gly	Thr	Ile	Arg	Lys	Gln	Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg	
65					70				75					80		
cag	agg	gtt	ctt	ttc	ctt	ctt	gat	ggc	tac	aat	gaa	ttc	aag	ccc	cag	288
Gln	Arg	Val	Leu	Phe	Leu	Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln	
			85					90						95		
aac	tgc	cca	gaa	atc	gaa	gcc	ctg	ata	aag	gaa	aac	cac	cgc	ttc	aag	336
Asn	Cys	Pro	Glu	Ile	Glu	Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys	
			100					105					110			
aac	atg	gtc	atc	gtc	acc	act	acc	act	gag	tgc	ctg	agg	cac	ata	cgg	384
Asn	Met	Val	Ile	Val	Thr	Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg	
			115					120					125			

179 891 DNA Homo sapiens CDS (1)...(891)

cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc 432  
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser  
130 135 140

gcc cag gct ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc 480  
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly  
145 150 155 160

ttg ttg ctc caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag 528  
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys  
165 170 175

acc cct ctc ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt 576  
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser  
180 185 190

gag ttc cac tct cac aca caa aca acg ctg ttc cat acc ttc tat gat 624  
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp  
195 200 205

ctg ttg ata cag aaa aac aaa cac aaa cat aaa ggt gtg gct gca agt 672  
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser  
210 215 220

gac ttc att cgg agc ctg gac cac cgt gga gac cta gct ctg gag ggt 720  
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly  
225 230 235 240

gtg ttc tcc cac aag ttt gat ttc gaa ctg cag gat gtg tcc agc gtg 768  
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val  
245 250 255

aat gag gat gtc ctg ctg aca act ggg ctc ctc tgt aaa tat aca gct 816  
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala  
260 265 270

caa agg ttc aag cca aag tat aaa ttc ttt cac aag tca ttc cag gag 864  
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu  
275 280 285

tac aca gca gga cga aga ctc agc agt 891  
Tyr Thr Ala Gly Arg Arg Leu Ser Ser  
290 295

<210> 180

<211> 297

<212> PRT

<213> Homo sapiens

<400> 180

Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser  
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CCDS: T23438.1

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Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
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Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
      50                55                60
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
      65                70                75                80
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
      85                90                95
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
      100               105               110
Asn Met Val Ile Val Thr Thr Thr Thr Glu Cys Leu Arg His Ile Arg
      115               120               125
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
      130               135               140
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
      145               150               155               160
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
      165               170               175
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
      180               185               190
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
      195               200               205
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
      210               215               220
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
      225               230               235               240
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
      245               250               255
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
      260               265               270
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
      275               280               285
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
      290               295

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<210> 181  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)...(618)

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Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
  1                5                10                15

aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg aag      96

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<210> 182
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<212> PRT
<213> Homo sapiens
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Leu Arg Leu Gln Ile Lys Arg  
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<210> 184  
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<212> PRT  
<213> Homo sapiens

<400> 184  
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln  
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Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn  
20 25 30  
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser  
35 40 45  
Leu Arg Leu Gln Ile Lys Arg  
50 55

<210> 185  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 185  
gaaatgtgct cgcaggagg 19

<210> 186  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 186  
gatgagcttc tgacaggccc 20

<210> 187  
<211> 3063  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)...(2385)  
  
<221> CDS  
<222> (2389)...(2928)

TC650T4260

<400> 187

tgt gaa atg tgc tgc cag gag gct ttt cag gca cag agg agc cag ctg	48
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu	
1 5 10 15	
gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg	96
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu	
20 25 30	
gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc	144
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly	
35 40 45	
ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg	192
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu	
50 55 60	
gac acc gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc atc gcg	240
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala	
65 70 75 80	
gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc	288
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly	
85 90 95	
tgc tgg gac ccc cac tgc ctc cac cca gcc cga gac ctg cag agt cac	336
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His	
100 105 110	
cgg cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg	384
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu	
115 120 125	
gac ctg gca tgg gag cgg ggt ttc gtc agc cag tat gaa tgt gat gaa	432
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu	
130 135 140	
atc agg ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt	480
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu	
145 150 155 160	
gat ctt gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa	528
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln	
165 170 175	
cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc	576
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala	
180 185 190	
aca tgc aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag	624
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln	
195 200 205	

TC649260

tct cgc ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag	672
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu	
210 215 220	
gac ata tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg	720
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met	
225 230 235 240	
gct gga ccc ccg cag aag agc cca gcc acc ctg ggc ctg gag gag ctc	768
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu	
245 250 255	
ttc agc acc cct ggc cac ctc aat gac gat gcg gac act gtg ctg gtg	816
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val	
260 265 270	
gtg ggt gag gcg ggc agt ggc aag agc acg ctc ctg cag cgg ctg cac	864
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His	
275 280 285	
ttg ctg tgg gct gca ggg caa gac ttc cag gaa ttt ctc ttt gtc ttc	912
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe	
290 295 300	
cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg	960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val	
305 310 315 320	
cgg act cta ctc ttt gag cac tgc tgt tgg cct gat gtt ggt caa gaa	1008
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu	
325 330 335	
gac atc ttc cag tta ctc ctt gac cac cct gac cgt gtc ctg tta acc	1056
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr	
340 345 350	
ttt gat ggc ttt gac gag ttc aag ttc agg ttc acg gat cgt gaa cgc	1104
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg	
355 360 365	
cac tgc tcc ccg acc gac ccc acc tct gtc cag acc ctg ctc ttc aac	1152
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn	
370 375 380	
ctt ctg cag ggc aac ctg ctg aag aat gcc cgc aag gtg gtg acc agc	1200
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser	
385 390 395 400	
cgt ccg gcc gct gtg tgc gcg ttc ctc agg aag tac atc cgc acc gag	1248
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu	
405 410 415	

1248-1250



Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys	
625 630 635 640	
gcc gag ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg	1968
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu	
645 650 655	
ttg tcc cgg gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag	2016
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu	
660 665 670	
aag gcc ctg ctc cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc	2064
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg	
675 680 685	
agc ctc cgc aag cac ttc cac tcc atc ccg cca gct gca ccg ggt gag	2112
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu	
690 695 700	
gcc aag agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc	2160
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser	
705 710 715 720	
ctg tac gag atg cag gag gag cgg ctg gct cgg aag gct gca cgt ggc	2208
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly	
725 730 735	
ctg aat gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act	2256
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr	
740 745 750	
gag tgt gct gcc ctg gcc ttt gtg ctg cag cac ctc cgg cgg ccc gtg	2304
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val	
755 760 765	
gcc ctg cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag	2352
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln	
770 775 780	
ctg ctg cct tgc ctt ggt gtc tgc aag gct ctg taa ttc tgg ggc aac	2400
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Phe Trp Gly Asn	
785 790 795	
aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat	2448
Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp	
800 805 810 815	
cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt	2496
His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser	
820 825 830	
gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta	2544
Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu	

835	840	845	
gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt			2592
Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys			
850	855	860	
tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aac			2640
Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Asn			
865	870	875	
ata aaa att cat gct tgc gga ttc aac aaa ctc ttg gaa agc att ttc			2688
Ile Lys Ile His Ala Ser Gly Phe Asn Lys Leu Leu Glu Ser Ile Phe			
880	885	890	895
tgc atc ctc ctg gtt gtg gaa gca ttt ttc ctg cag aaa gtt gtc aag			2736
Cys Ile Leu Leu Val Val Glu Ala Phe Phe Leu Gln Lys Val Val Lys			
900	905	910	
att ctt gaa gaa atg gta gtc agt tgg cta gag gtc agg ttg tcc aat			2784
Ile Leu Glu Glu Met Val Val Ser Trp Leu Glu Val Arg Leu Ser Asn			
915	920	925	
aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa			2832
Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu			
930	935	940	
agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc tct			2880
Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe Ser			
945	950	955	
cta gag gag gtt gac aag ctc ggc tgc agg gac acc aga ctc ttg ctt			2928
Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr Arg Leu Leu Leu			
960	965	970	975
tgaagtctcc gggaggatgt tcgtctcagt ttgtttgtga gcaggctgtg agtttgggcc			2988
ccagaggctg ggtgacatgt gttggcagcc tcttcaaaat gagccctgtc ctgcctaagg			3048
ctgaacttgt tttct			3063

<210> 188  
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 <212> PRT  
 <213> Homo sapiens

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 Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly  
 35 40 45  
 Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu  
 50 55 60  
 Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala

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65				70				75				80			
Ala	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ser	Gln	Ser	Pro	Lys	Leu	His	Gly
				85					90				95		
Cys	Trp	Asp	Pro	His	Ser	Leu	His	Pro	Ala	Arg	Asp	Leu	Gln	Ser	His
			100					105					110		
Arg	Pro	Ala	Ile	Val	Arg	Arg	Leu	His	Ser	His	Val	Glu	Asn	Met	Leu
		115					120					125			
Asp	Leu	Ala	Trp	Glu	Arg	Gly	Phe	Val	Ser	Gln	Tyr	Glu	Cys	Asp	Glu
	130					135					140				
Ile	Arg	Leu	Pro	Ile	Phe	Thr	Pro	Ser	Gln	Arg	Ala	Arg	Arg	Leu	Leu
145					150					155					160
Asp	Leu	Ala	Thr	Val	Lys	Ala	Asn	Gly	Leu	Ala	Ala	Phe	Leu	Leu	Gln
				165					170						175
His	Val	Gln	Glu	Leu	Pro	Val	Pro	Leu	Ala	Leu	Pro	Leu	Glu	Ala	Ala
			180					185					190		
Thr	Cys	Lys	Lys	Tyr	Met	Ala	Lys	Leu	Arg	Thr	Thr	Val	Ser	Ala	Gln
		195						200				205			
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu
	210					215					220				
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met
225					230					235					240
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu
				245					250						255
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val
			260					265					270		
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His
	275						280					285			
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe
	290					295					300				
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val
305					310					315					320
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu
				325					330						335
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr
			340					345					350		
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg
	355						360					365			
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn
	370					375						380			
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser
385					390					395					400
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu
				405					410						415
Phe	Asn	Leu	Lys	Gly	Phe	Ser	Glu	Gln	Gly	Ile	Glu	Leu	Tyr	Leu	Arg
		420						425					430		
Lys	Arg	His	His	Glu	Pro	Gly	Val	Ala	Asp	Arg	Leu	Ile	Arg	Leu	Leu
		435					440						445		
Gln	Glu	Thr	Ser	Ala	Leu	His	Gly	Leu	Cys	His	Leu	Pro	Val	Phe	Ser
	450					455					460				
Trp	Met	Val	Ser	Lys	Cys	His	Gln	Glu	Leu	Leu	Leu	Gln	Glu	Gly	Gly
465					470					475					480
Ser	Pro	Lys	Thr	Thr	Thr	Asp	Met	Tyr	Leu	Leu	Ile	Leu	Gln	His	Phe
				485					490						495

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Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
      500                      505                      510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
      515                      520                      525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
      530                      535                      540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545                      550                      555                      560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
      565                      570                      575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
      580                      585                      590
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
      595                      600                      605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
      610                      615                      620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625                      630                      635                      640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
      645                      650                      655
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
      660                      665                      670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
      675                      680                      685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
      690                      695                      700
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705                      710                      715                      720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
      725                      730                      735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
      740                      745                      750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
      755                      760                      765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
      770                      775                      780
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu
785                      790                      795

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<210> 189  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
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 1 5 10 15  
 Ala Leu Gly Asp His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn  
 20 25 30  
 Asn Ile Gly Ser Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys  
 35 40 45  
 Asn Val Met Leu Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp



Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala  
80 85 90

cag gag gct gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt 519  
Gln Glu Ala Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe  
95 100 105

tgc aga gtg ggc cct gca gag tgt gct gca ctg gcc ttt gta ctg caa 567  
Cys Arg Val Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln  
110 115 120 125

cat ctc cag cgg cct gtg gcc cta cag ctg gat tac aac tct gtg 612  
His Leu Gln Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val  
130 135 140

ggagatgttg ggagtggaaac agctgacgacc gtgccttttg ggtctgcaca gctctgtagt 672  
gagtgtagaca aggtcttgcc gattgggcct gtggcaaata ctactgtca 721

<210> 191  
<211> 140  
<212> PRT  
<213> Mus musculus

<400> 191  
Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu  
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Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln  
20 25 30  
Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys  
35 40 45  
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val  
50 55 60  
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu  
65 70 75 80  
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala  
85 90 95  
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val  
100 105 110  
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln  
115 120 125  
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val  
130 135 140

<210> 192  
<211> 419  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1)...(417)

CCDS: Mus musculus



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<210> 194
<211> 26
<212> DNA
<213> Artificial Sequence
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<220>  
<223> primer

<400> 194  
ctgcagaagg ctgagccaca caacct 26

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<210> 195
<211> 30
<212> DNA
<213> Artificial Sequence
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<220>  
<223> primer

<400> 195  
acagagttgt aatccagctg tagggccaca 30